162174

STIC-Biotech/ChemLib

From: Bowman, Amy
Sent: Wednesday, September 28, 2005 3:01 PM
To: STIC-Biotech/ChemLib
Cc: Bowman, Amy
Subject: sequence search-10/738,413

Hello,
I need SEQ ID NO: 1 searched in application 10/738,413, with lower and upper limits of 21 and 30 nucleobases, respectively.
Thank you,
Amy Bowman
AU 1635
REM 2C31
mail REM 2C18
571-272-0755

CRTE

Barb O Byer

****
Searcher:_____
Searcher Phone:_____
Date Searcher Picked up:_____
Date completed:_____
Searcher Prep Time:_____
Online Time:_____

****
Type of Search
NA#_____ AA#:_____
S/L:_____ Oligomer:_____
Encode/Transl:_____
Structure #:_____Text:____
Inventor:_____ Litigation:___

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other (Specify):_____

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 30, 2005, 09:06:54 ; Search time 1712 Seconds
(without alignments)
594.369 Million cell updates/sec

Title: US-10-738-413-1
Perfect score: 21
Sequence: 1 uaggaccugccagugcucutt 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 646394

Minimum DB seq length: 21
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	13.6	64.8	26	6	AR091153	AR091153 Sequence
2	13.6	64.8	26	6	AR091206	AR091206 Sequence
c 3	13.6	64.8	26	6	AR198188	AR198188 Sequence
4	13.6	64.8	26	6	AR198241	AR198241 Sequence
c 5	13.6	64.8	26	6	AR260342	AR260342 Sequence
6	13.6	64.8	26	6	AR260395	AR260395 Sequence
c 7	13.4	63.8	23	6	AR526958	AR526958 Sequence
8	13.4	63.8	25	6	I28239	I28239 Sequence 15
9	13.4	63.8	25	6	AR195002	AR195002 Sequence
10	13.4	63.8	29	6	AX183809	AX183809 Sequence
c 11	13.2	62.9	22	6	E26686	E26686 Improved me
12	13.2	62.9	24	6	AX292533	AX292533 Sequence
13	12.8	61.0	21	6	BD171375	BD171375 Method fo
14	12.8	61.0	21	6	BD173609	BD173609 Method of
c 15	12.8	61.0	22	6	AX354409	AX354409 Sequence
16	12.8	61.0	25	6	CQ866237	CQ866237 Sequence
c 17	12.6	60.0	22	6	AX503893	AX503893 Sequence
c 18	12.6	60.0	23	6	AX148231	AX148231 Sequence
19	12.6	60.0	23	6	AX473373	AX473373 Sequence
c 20	12.6	60.0	30	6	AR091140	AR091140 Sequence
c 21	12.6	60.0	30	6	AR198175	AR198175 Sequence
c 22	12.6	60.0	30	6	AR260329	AR260329 Sequence
23	12.4	59.0	22	6	AR093096	AR093096 Sequence
24	12.4	59.0	22	6	BD009920	BD009920 BH3 inter
25	12.4	59.0	23	6	E10819	E10819 FITC labeli
c 26	12.4	59.0	28	6	AX614457	AX614457 Sequence
c 27	12.2	58.1	22	6	AR093407	AR093407 Sequence
28	12.2	58.1	22	6	AR179499	AR179499 Sequence
c 29	12.2	58.1	22	6	E30932	E30932 Amplificati
30	12.2	58.1	23	6	AR225080	AR225080 Sequence
31	12.2	58.1	24	6	AX290310	AX290310 Sequence
c 32	12.2	58.1	25	6	E52191	E52191 Novel gene
c 33	12.2	58.1	29	6	BD170056	BD170056 Novel N-a
c 34	12.2	58.1	30	10	S86546	S86546 TCR V beta
c 35	12	57.1	21	6	AR123316	AR123316 Sequence
c 36	12	57.1	21	6	AR487412	AR487412 Sequence
37	12	57.1	21	6	AR529674	AR529674 Sequence
38	12	57.1	21	6	AX095699	AX095699 Sequence
c 39	12	57.1	23	6	AX105351	AX105351 Sequence
c 40	12	57.1	24	6	CQ792973	CQ792973 Sequence
c 41	12	57.1	25	6	AR117096	AR117096 Sequence
42	12	57.1	25	6	AR175422	AR175422 Sequence
43	12	57.1	25	6	AR238776	AR238776 Sequence
c 44	12	57.1	25	6	AR338139	AR338139 Sequence
c 45	12	57.1	25	6	AX609748	AX609748 Sequence

ALIGNMENTS

RESULT 1
AR091153/c
LOCUS AR091153 26 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 1273 from patent US 5994076.
ACCESSION AR091153
VERSION AR091153.1 GI:10017908
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 5994076-A 1273 30-NOV-1999;
FEATURES Location/Qualifiers
source 1. .26
/organism="unknown"
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ORIGIN

Query Match 64.8%; Score 13.6; DB 6; Length 26;
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Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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Db         20 TTGGCCTTGCCGGTGCTCTT 1
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RESULT 2
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LOCUS AR091206 26 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 1326 from patent US 5994076.
ACCESSION AR091206
VERSION AR091206.1 GI:10017961
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression

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  JOURNAL   Patent: US 5994076-A 1326 30-NOV-1999;
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ORIGIN

  Query Match             64.8%;  Score 13.6;  DB 6;  Length 26;
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Qy          2 AGGACCUGCCAGUGCUCUTT 21
              |||||| |||| |:  ||
Db          4 AGGACCTTCCAGTCCTACTT 23


RESULT 3
AR198188/c
LOCUS       AR198188                  26 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 1273 from patent US 6352829.
ACCESSION   AR198188
VERSION     AR198188.1  GI:20248037
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
  TITLE     Methods of assaying differential expression
  JOURNAL   Patent: US 6352829-A 1273 05-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .26
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ORIGIN

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  Matches   11;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 UAGGACCUGCCAGUGCUCUT 20
              : || | :||| |:||:|:|
Db         20 TTGGCCTTGCCGGTGCTCTT 1


RESULT 4
AR198241
LOCUS       AR198241                  26 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 1326 from patent US 6352829.
ACCESSION   AR198241
VERSION     AR198241.1  GI:20248090
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
  TITLE     Methods of assaying differential expression
  JOURNAL   Patent: US 6352829-A 1326 05-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .26
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ORIGIN

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  Matches   13;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 AGGACCUGCCAGUGCUCUTT 21
              |||||| |||| |:  ||
Db          4 AGGACCTTCCAGTCCTACTT 23


RESULT 5
AR260342/c
LOCUS       AR260342                  26 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 1273 from patent US 6489455.
ACCESSION   AR260342
VERSION     AR260342.1  GI:27310853
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
  TITLE     Methods of assaying differential expression
  JOURNAL   Patent: US 6489455-A 1273 03-DEC-2002;
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  Matches   11;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 UAGGACCUGCCAGUGCUCUT 20
              : || | :||| |:||:|:|
Db         20 TTGGCCTTGCCGGTGCTCTT 1


RESULT 6
AR260395
LOCUS       AR260395                  26 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 1326 from patent US 6489455.
ACCESSION   AR260395
VERSION     AR260395.1  GI:27310906
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
  TITLE     Methods of assaying differential expression
  JOURNAL   Patent: US 6489455-A 1326 03-DEC-2002;
FEATURES             Location/Qualifiers
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Qy          2 AGGACCUGCCAGUGCUCUTT 21
              |||||| |||| |:  ||
Db          4 AGGACCTTCCAGTCCTACTT 23


RESULT 7
AR526958/c
LOCUS       AR526958                  23 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 12 from patent US 6723534.
ACCESSION   AR526958
VERSION     AR526958.1  GI:53913871
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Lin,H.
  TITLE     Purified and isolated PIWI family genes and gene products and
            therapeutic and screening methods using same
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  JOURNAL   Patent: US 6723534-A 12 20-APR-2004;
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Qy          2 AGGACCUGCCAGUGC 16
              |||||||:| |||:||
Db         16 AGGACCTGGCAGTGC 2


RESULT 8
I28239
LOCUS       I28239                    25 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 15 from patent US 5569753.
ACCESSION   I28239
VERSION     I28239.1  GI:1819015
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Wigler,M. and Lisitsyn,N.
  TITLE     Cancer detection probes
  JOURNAL   Patent: US 5569753-A 15 29-OCT-1996;
FEATURES             Location/Qualifiers
     source          1. .25
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ORIGIN

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Qy          1 UAGGACCUGCCAGUG 15
              :|||| |:|||||:|
Db          3 TAGGAACTGCCAGTG 17


RESULT 9
AR195002
LOCUS       AR195002                  25 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 24 from patent US 6350576.
ACCESSION   AR195002
VERSION     AR195002.1  GI:20244439
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Wigler,M. and Lisitsyn,N.
  TITLE     Cancer detection probes
  JOURNAL   Patent: US 6350576-A 24 26-FEB-2002;
FEATURES             Location/Qualifiers
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ORIGIN

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Qy          1 UAGGACCUGCCAGUG 15
              :|||| |:|||||:|
Db          3 TAGGAACTGCCAGTG 17


RESULT 10
AX183809
LOCUS       AX183809                  29 bp    DNA     linear   PAT 06-AUG-2001
DEFINITION  Sequence 1562 from Patent WO0142511.
ACCESSION   AX183809
VERSION     AX183809.1  GI:15135137
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Daly,M., Hudson,T.J., Lander,E.S., Rioux,J. and Siminovitch,K.
  TITLE     Ibd-related polymorphisms
  JOURNAL   Patent: WO 0142511-A 1562 14-JUN-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis
            Biotherapeutics Corporation (CA)
FEATURES             Location/Qualifiers
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ORIGIN

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Qy          2 AGGACCUGCCAGUGCU 17
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Db         10 AGGANCTGACAGTGCT 25


RESULT 11
E26686/c
LOCUS       E26686                    22 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Improved method for measuring cytokine gene expression.
ACCESSION   E26686
VERSION     E26686.1  GI:13026273
KEYWORDS    JP 1999155600-A/36.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Michio,S., Takeshi,H., Masato,H. and Hideyuki,I.
  TITLE     Improved method for measuring cytokine gene expression
  JOURNAL   Patent: JP 1999155600-A 36 15-JUN-1999;
            SHISEIDO CO LTD
COMMENT     OS   Unidentified
            PN   JP 1999155600-A/36
            PD   15-JUN-1999
            PF   28-NOV-1997 JP 1997328171
            PR
            PI   MICHIO SHIBATA,TAKESHI HARIYA,MASATO HATAO,HIDEYUKI ICHIKAWA
            PC   C12Q1/68,C07K14/52,C07K14/54,C07K14/55,C07K14/56,C07K14/57, PC
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RESULT 12
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LOCUS       AX292533                 24 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 4295 from Patent WO0179548.
ACCESSION   AX292533
VERSION     AX292533.1  GI:17054216
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
  TITLE     Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
  JOURNAL   Patent: WO 0179548-A 4295 25-OCT-2001;
            CORNELL RESEARCH FOUNDATION, INC. (US)
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ORIGIN

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Qy          3 GGACCUGCCAGUGCUCUT 20
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Db          7 GGACCTGGTAGTGCTCGT 24


RESULT 13
BD171375
LOCUS       BD171375                 21 bp    DNA     linear   PAT 18-FEB-2003
DEFINITION  Method for detecting bronchial asthma risk factor.
ACCESSION   BD171375
VERSION     BD171375.1  GI:28412665
KEYWORDS    JP 2002218997-A/10.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Nakamura,Y. and Tamari,M.
  TITLE     Method for detecting bronchial asthma risk factor
  JOURNAL   Patent: JP 2002218997-A 10 06-AUG-2002;
            OTSUKA PHARMACEUTICAL CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002218997-A/10
            PD   06-AUG-2002
            PF   25-JAN-2001 JP 2001017076
            PI   YUSUKE NAKAMURA,MAYUMI TAMARI
            PC   C12Q1/68,C12N15/09,C12N15/00
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  Matches   10;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

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Db          5 ACCTGCCAGTGTTTTT 20


RESULT 14
BD173609
LOCUS       BD173609                 21 bp    DNA     linear   PAT 18-FEB-2003
DEFINITION  Method of detecting bronchial asthma onset risk factor.
ACCESSION   BD173609
VERSION     BD173609.1  GI:28414940
KEYWORDS    WO 02059305-A/10.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Nakamura,Y. and Tamari,M.
  TITLE     Method of detecting bronchial asthma onset risk factor
  JOURNAL   Patent: WO 02059305-A 10 01-AUG-2002;
            OTSUKA PHARMACEUTICAL CO LTD,YUSUKE NAKAMURA,MAYUMI TAMARI
COMMENT     OS   Artificial Sequence
            PN   WO 02059305-A/10
            PD   01-AUG-2002
            PF   25-JAN-2002 WO 2002JP000540
            PR   25-JAN-2001 JP 01P   017076
            PI   YUSUKE NAKAMURA,MAYUMI TAMARI
            PC   C12N15/12,C12Q1/68,G01N33/53
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RESULT 15
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LOCUS       AX354409                 22 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 55 from Patent WO0196523.
ACCESSION   AX354409
VERSION     AX354409.1  GI:18619251
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kennedy,G.C., Kang,S., Reinhard,C. and Jefferson,A.B.
  TITLE     Polynucleotides related to colon cancer
  JOURNAL   Patent: WO 0196523-A 55 20-DEC-2001;
            CHIRON CORPORATION (US)
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Best Local Similarity 62.5%; Pred. No. 4.2e+04;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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Job time : 1716 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 30, 2005, 09:06:54 ; Search time 415 Seconds
(without alignments)
299.553 Million cell updates/sec

Title: US-10-738-413-1
Perfect score: 21
Sequence: 1 uaggaccugccagugcucutt 21

Scoring table: IDENTITY_NUC
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Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 1315584

Minimum DB seq length: 21
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	14.6	69.5	28	4	AAH74915	Aah74915 DNA seque
c	2	14.2	67.6	25	9	ACI63698	Aci63698 Human mic
	3	14.2	67.6	28	10	AAD51155	Aad51155 Adapter D
	4	14.2	67.6	30	12	ADP45901	Adp45901 PCR prime
	5	13.8	65.7	22	12	ADK94415	Adk94415 Primer of
c	6	13.8	65.7	23	5	AAD02074	Aad02074 3' PCR pr
c	7	13.8	65.7	25	9	ACK21937	Ack21937 Human mic
c	8	13.8	65.7	25	9	ACI58170	Aci58170 Human mic
	9	13.8	65.7	29	10	ADC47044	Adc47044 BEC1 pota
	10	13.8	65.7	29	10	ADI35763	Adi35763 Human pot
c	11	13.6	64.8	26	6	ABK67185	Abk67185 Human gen
	12	13.6	64.8	26	6	ABK67238	Abk67238 Human gen
	13	13.6	64.8	28	10	AAD51147	Aad51147 Adapter D
	14	13.4	63.8	25	2	AAT32267	Aat32267 Probe for
	15	13.4	63.8	25	2	AAT71677	Aat71677 Cancer de
	16	13.4	63.8	29	4	AAH91238	Aah91238 Human inf
c	17	13.2	62.9	22	2	AAX78420	Aax78420 Rat GADPH
c	18	13.2	62.9	22	2	AAX25938	Aax25938 IL12 p35
c	19	13.2	62.9	24	6	ABI90987	Abi90987 Capture o
	20	13.2	62.9	24	6	ABI90986	Abi90986 Capture o
	21	13.2	62.9	30	4	AAS05688	Aas05688 Human pro
	22	13.2	62.9	30	8	ACC80639	Acc80639 Human pro
	23	12.8	61.0	21	6	AAL44199	Aal44199 Human I-k
c	24	12.8	61.0	22	6	AAL41637	Aal41637 Human col
c	25	12.8	61.0	25	9	ACI01231	Aci01231 Human mic
c	26	12.8	61.0	25	10	ADC51559	Adc51559 Primer re
	27	12.8	61.0	25	13	ADR57519	Adr57519 Drug ther
	28	12.8	61.0	26	10	ADE40061	Ade40061 5' TET an
	29	12.8	61.0	26	10	ADE40067	Ade40067 5' TET an
	30	12.8	61.0	26	10	ADE40055	Ade40055 5' TET an
	31	12.8	61.0	26	10	ADG14352	Adg14352 Human G-p
	32	12.6	60.0	21	9	AAD58127	Aad58127 GAPDH spe
	33	12.6	60.0	21	10	ADD44397	Add44397 Rat GAPDH
c	34	12.6	60.0	22	6	ABS63481	Abs63481 Real-time
c	35	12.6	60.0	23	5	AAS07986	Aas07986 Human G-p
	36	12.6	60.0	23	6	ABA94688	Aba94688 GAPDH RNA
c	37	12.6	60.0	23	11	ADL96518	Adl96518 Human G p
c	38	12.6	60.0	23	12	ADQ37704	Adq37704 Human G-p
c	39	12.6	60.0	25	9	ACC42118	Acc42118 Human KCN
c	40	12.6	60.0	25	9	ACI13346	Aci13346 Human mic
c	41	12.6	60.0	25	9	ACI99906	Aci99906 Human mic
c	42	12.6	60.0	25	9	ACI63080	Aci63080 Human mic
	43	12.6	60.0	25	9	ACI01867	Aci01867 Human mic
c	44	12.6	60.0	25	9	ACI63699	Aci63699 Human mic
c	45	12.6	60.0	30	6	ABK67172	Abk67172 Human gen

ALIGNMENTS

RESULT 1
AAH74915
ID AAH74915 standard; DNA; 28 BP.
XX
AC AAH74915;
XX
DT 29-OCT-2001 (first entry)
XX
DE DNA sequence of encoded adaptor for detecting base 1 of template.
XX
KW Nucleotide sequence signature; nucleotide sequencing; ss.
XX
OS Synthetic.
XX
PN WO200161044-A1.
XX
PD 23-AUG-2001.
XX
PF 15-FEB-2001; 2001WO-US005032.
XX
PR 15-FEB-2000; 2000US-0182454P.
PR 01-SEP-2000; 2000US-0654187P.
XX
PA (LYNX-) LYNX THERAPEUTICS INC.
XX
PI Corcoran KC, Eletr S;
XX
DR WPI; 2001-522608/57.
XX
PT Determining nucleotide sequence signature, by obtaining optical values
PT for each nucleotide position in a group, adjusting them to get ratio of
PT final highest values near predetermined factor, generating base call.
XX
PS Disclosure; Page 15; 73pp; English.
XX
CC The specification describes a method for determining a nucleotide
CC sequence signature. The method comprises obtaining optical measurements
CC with values indicating each nucleotide in a group of nucleotide
CC positions, adjusting the values until the ratio of highest value in the
CC set to next highest values in the set is at least a predetermined factor,
CC and generating a base call for a position in the group based on results
CC after the adjustment of values. The method is used for determining a
CC signature of a nucleotide sequence, and for determining a nucleotide

```
CC   sequence of a polynucleotide from a series of optical measurements.
CC   AAH74912-27 represent encoded adaptors, which are used for detecting
CC   bases of a DNA template, in the course of the invention
XX
SQ   Sequence 28 BP; 4 A; 7 C; 7 G; 7 T; 0 U; 3 Other;

  Query Match             69.5%;  Score 14.6;  DB 4;  Length 28;
  Best Local Similarity   61.9%;  Pred. No. 2.8e+03;
  Matches   13;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 UAGGACCUGCCAGUGCUCUTT 21
              :| || |:|||||: | |:||
Db          4 TACGAGCTGCCAGTCCGCTTT 24


RESULT 2
ACI63698/c
ID   ACI63698 standard; DNA; 25 BP.
XX
AC   ACI63698;
XX
DT   13-OCT-2003  (first entry)
XX
DE   Human microarray DNA oligonucleotide SEQ ID NO 63689.
XX
KW   EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW   genetic variation; biallelic marker; polymorphism; human;
KW   cross-species comparison.
XX
OS   Homo sapiens.
XX
PN   US2003104410-A1.
XX
PD   05-JUN-2003.
XX
PF   15-MAR-2002; 2002US-00098263.
XX
PR   16-MAR-2001; 2001US-0276759P.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Mittmann MP;
XX
DR   WPI; 2003-567953/53.
XX
PT   New array of nucleic acid probes, useful for in situ hybridization, in
PT   Southern, Northern or dot-blot hybridization to identify or detect the
PT   sequence or specific mutations of any gene.
XX
PS   Claim 1; SEQ ID NO 63689; 9pp; English.
XX
CC   The invention discloses a microarray comprising a plurality of nucleic
CC   acid probes including one of 2,018,500 fully defined sequences, or its
CC   perfect match, perfect mismatch, antisense match or antisense mismatch.
CC   Also disclosed is a method of gene expression analysis. The array is used
CC   in monitoring gene expression levels by hybridisation to a DNA library,
CC   in analysis of genetic variation or in hybridisation of tag-labelled
CC   compounds. The nucleic acid probes are specifically designed for analysis
CC   of at least one target sequence. The method of analysis comprises
CC   hybridising at least one or more nucleic acids to at least two or more
CC   nucleic acid probes and detecting the hybridisation. The nucleic acid
CC   probes are attached to a solid support. The analysis comprises monitoring
CC   gene expression levels, identifying biallelic markers or polymorphisms,
CC   or family members of a gene and a cross-species comparison. Each of the
CC   nucleic acids further comprises a tag sequence. The array of nucleic acid
CC   probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC   blot hybridisation to identify or detect the sequence or specific
CC   mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC   primer extensions or in screening cDNA or genomic libraries or subclones
CC   for additional subclones containing segments of DNA that have been
CC   isolated and previously sequenced. The sequence presented is one of the
CC   nucleic acid probes incorporated in the microarray. Note: The sequence
CC   data for this patent can also be obtained in electronic format directly
CC   from USPTO at seqdata.uspto.goc/sequence.html
XX
SQ   Sequence 25 BP; 8 A; 5 C; 4 G; 8 T; 0 U; 0 Other;

  Query Match             67.6%;  Score 14.2;  DB 9;  Length 25;
  Best Local Similarity   63.2%;  Pred. No. 4.3e+03;
  Matches   12;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 GGACCUGCCAGUGCUCUTT 21
              ||| |:| |||:| :|:||
Db         24 GGAACTGACAGTGTTCTTT 6


RESULT 3
AAD51155
ID   AAD51155 standard; DNA; 28 BP.
XX
AC   AAD51155;
XX
DT   02-APR-2003  (first entry)
XX
DE   Adapter DNA #10 used to illustrate the method of the invention.
XX
KW   Genetic analysis; allelic analysis; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    4
FT                   /*tag=  a
FT                   /note= "Represented as X2 in the specification"
XX
PN   WO200279496-A2.
XX
PD   10-OCT-2002.
XX
PF   27-MAR-2002; 2002WO-US009928.
XX
PR   28-MAR-2001; 2001US-00821694.
XX
PA   (MIND-) APPLIED MINDS INC.
XX
PI   Hillis WD;
XX
DR   WPI; 2003-046825/04.
XX
PT   Obtaining information on target nucleic acid analyte, by hybridizing
PT   target with oligonucleotide probes complementary, or complementary except
PT   at position of interest to target and analyzing probe hybridization.
XX
PS   Example 1; Page 39; 66pp; English.
XX
CC   The invention relates to a method of obtaining information on a target
CC   nucleic acid analyte containing a target segment. The method involves
CC   hybridising target nucleic acid analyte with at least two oligonucleotide
CC   probes, where each probe comprises a sequence fully complementary, or
CC   complementary except at a position of interest or variable position, to
CC   the target nucleic acid analyte and analysing whether all, some or none
CC   of the probes hybridise. The method is useful for sequencing and for
CC   obtaining information on a number of target nucleic acid sequence
CC   segments, where information comprises the determination of a nucleotide
CC   at a position of interest. It is also useful for genetic or allelic
CC   analysis of genomic DNA or cDNA. The present sequence is an adapter DNA,
CC   used to illustrate the method of the invention
XX
SQ   Sequence 28 BP; 4 A; 7 C; 7 G; 6 T; 0 U; 4 Other;

  Query Match             67.6%;  Score 14.2;  DB 10;  Length 28;
  Best Local Similarity   61.9%;  Pred. No. 4.4e+03;
  Matches   13;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 UAGGACCUGCCAGUGCUCUTT 21
              :| || |:|||||: | |:||
```

```
Db          4 KACGAGCTGCCAGTCCGCTTT 24


RESULT 4
ADP45901
ID   ADP45901 standard; DNA; 30 BP.
XX
AC   ADP45901;
XX
DT   26-AUG-2004  (first entry)
XX
DE   PCR primer 4 used to genotype human MAP kinase MAPK10 polymorphism.
XX
KW   breast cancer; cytostatic; gene therapy; human; ss; primer; PCR; SNP;
KW   single nucleotide polymorphism; MAP kinase; MAPK10; JNK3; JNK3A; p493F12;
KW   p54bSAPK MAP kinase; c-Jun kinase 3; JNK3 alpha protein kinase;
KW   c-Jun N-terminal kinase 3; stress activated protein kinase beta;
KW   chromosome 4q22.1-q23.
XX
OS   Homo sapiens.
XX
PN   WO2004047623-A2.
XX
PD   10-JUN-2004.
XX
PF   25-NOV-2003; 2003WO-US037948.
XX
PR   25-NOV-2002; 2002US-0429136P.
PR   24-JUL-2003; 2003US-0490234P.
XX
PA   (SEQU-) SEQUENOM INC.
XX
PI   Roth RB,  Nelson MR,  Braun A,  Kammerer SM,  Reneland R;
XX
DR   WPI; 2004-441051/41.
XX
PT   Identifying a subject at risk of breast cancer by detecting the presence
PT   of polymorphic variations in the ICAM, MAPK10, KIAA0861, NUMA1 or GALE
PT   regions which are associated with breast cancer in a nucleic acid sample
PT   from a subject.
XX
PS   Example 5; Page 90; 289pp; English.
XX
CC   The invention relates to a novel method for identifying a subject at risk
CC   of breast cancer comprising detecting the presence or absence of one or
CC   more polymorphic variations associated with breast cancer in a nucleic
CC   acid sample from a subject. The method of the invention has cytostatic
CC   applications and may be useful for identifying a subject at risk of
CC   breast cancer, for early diagnosis, prevention and treatment of breast
CC   cancer, possibly via gene therapy, as well as to analyse and predict a
CC   response to a breast cancer treatment and in clinical drug trials. The
CC   current sequence is that of a PCR primer of the invention which was used
CC   to genotype human MAP kinase MAPK10 (JNK3;JNK3A;p493F12;p54bSAPK MAP
CC   kinase;c-Jun kinase 3;JNK3 alpha protein kinase;c-Jun N-terminal kinase 3
CC   ;stress activated protein kinase beta) gDNA which has been mapped to
CC   chromosomal position 4q22.1-q23.
XX
SQ   Sequence 30 BP; 7 A; 6 C; 9 G; 8 T; 0 U; 0 Other;

  Query Match             67.6%;  Score 14.2;  DB 12;  Length 30;
  Best Local Similarity   57.9%;  Pred. No. 4.4e+03;
  Matches   11;  Conservative    5;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 UAGGACCUGCCAGUGCUCU 19
              : |||  :|||||:||:|:
Db          4 TTGGATGTGCCAGTGCTCT 22


RESULT 5
ADK94415
ID   ADK94415 standard; DNA; 22 BP.
XX
AC   ADK94415;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Primer of the invention #135.
XX
KW   human; single nucleotide polymorphism; SNP; ss; primer.
XX
OS   Synthetic.
XX
PN   JP2003259875-A.
XX
PD   16-SEP-2003.
XX
PF   08-MAR-2002; 2002JP-00064373.
XX
PR   08-MAR-2002; 2002JP-00064373.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2004-093977/10.
XX
PT   Novel polynucleotide useful for PCR amplification along with two DNA
PT   fragment from another set of sequences, or for detecting single
PT   nucleotide polymorphism in human gene.
XX
PS   Claim 2; SEQ ID NO 3444; 2627pp; Japanese.
XX
CC   The present invention relates to a polynucleotide isolated from a human
CC   gene and is useful for detecting a single nucleotide polymorphism in a
CC   human gene or for diagnosing of disease. The invention enables the
CC   detection of a single nucleotide polymorphism in a human gene. The
CC   present sequence represents a primer of the invention.
XX
SQ   Sequence 22 BP; 3 A; 7 C; 5 G; 7 T; 0 U; 0 Other;

  Query Match             65.7%;  Score 13.8;  DB 12;  Length 22;
  Best Local Similarity   64.7%;  Pred. No. 6.7e+03;
  Matches   11;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 UAGGACCUGCCAGUGCU 17
              :|||| |: ||||:||:
Db          4 TAGGATCTTCCAGTGCT 20


RESULT 6
AAD02074/c
ID   AAD02074 standard; DNA; 23 BP.
XX
AC   AAD02074;
XX
DT   26-MAR-2001  (first entry)
XX
DE   3' PCR primer for preparing N-myc fusion construct.
XX
KW   Human; tumour necrosis factor; TNF; TRAF2; inhibitor; treatment;
KW   TNF-receptor associated factor; TRAF2 truncated; TRAF2TR; TRAF2TD;
KW   TRAF2 truncated-deleted; antiinflammatory; cardiant; Myc tag; vasotropic;
KW   antipsoriatic; antirheumatic; antiarthritic; antidiabetic;
KW   antiarteriosclerotic; immunosuppressive; Crohn's disease; psoriasis;
KW   rheumatoid arthritis; graft versus host disease; cardiovascular disease;
KW   non-insulin dependent diabetes; inflammatory bowel disease; stroke;
KW   neurodegenerative disease; congestive heart failure; PCR primer;
KW   myocardial infarction; nuclear factor kappa B; NFkB; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200066737-A1.
XX
PD   09-NOV-2000.
XX
PF   06-APR-2000; 2000WO-US009178.
XX
```

PR 30-APR-1999; 99US-0131940P.
XX
PA (AVET) AVENTIS PHARM PROD INC.
XX
PI Searfoss GH, Pagnoni MF, Ivashchenko YD, Guo K, Clark KL;
XX
DR WPI; 2001-007223/01.
XX
PT New nucleic acid encoding variants of tumor necrosis factor receptor
PT associated factors useful for inhibiting tumor necrosis factor alpha-
PT regulated pathways, and for treating Crohn's disease, psoriasis, and
PT rheumatoid arthritis.
XX
PS Example 3; Page 42; 74pp; English.
XX
CC The present invention relates to variants of tumour necrosis factor (TNF)
CC -receptor associated factor (TRAF2). TRAF2 has two variants, a splice
CC variant referred as "TRAF2 truncated" (TRAF2TR) and an expression
CC construct with enhanced dominant negative properties referred as "TRAF2
CC truncated-deleted" (TRAF2TD). TRAF2 variants are capable of inhibiting
CC TNF alpha signalling pathways and for inhibiting diseases involving over
CC production of TNFalpha, TNFalpha pathologies involving hyperactivation of
CC nuclear factor kappa B (NFkB). The variants are also useful for
CC inhibiting and treating inflammatory processes involving TNFalpha such as
CC Crohn's disease, psoriasis, rheumatoid arthritis, graft versus host
CC disease, non-insulin dependent diabetes, inflammatory bowel disease, and
CC neurodegenerative diseases or cardiovascular disease such as cardiac
CC ischaemia-reperfusion injury following myocardial infarction, coronary
CC artery bypass surgery, cardiac transplantation or ischaemia-reperfusion
CC injury in the central nervous system (CNS) following stroke, the
CC progression and rupture of advanced coronary atherosclerotic plaques,
CC development and progression of congestive heart failure, endothelial cell
CC injury following balloon angioplasty, or apoptotic cell death of
CC myocardial cells. The present sequence is a 3' PCR primer for preparing a
CC fusion construct containing N-myc affinity tag as well as truncated and
CC full length TRAF2. N-myc is useful for determining the effect of TRAF2TR
CC on NFkB activation. Truncated as well as full length TRAF2 were
CC constructed with N-Myc affinity tags in a mammalian expression vector
CC (pcDNA3). N-myc fusion constructs were prepared using 5' and 3' PCR
CC primers
XX
SQ Sequence 23 BP; 6 A; 7 C; 5 G; 5 T; 0 U; 0 Other;

```
  Query Match             65.7%;  Score 13.8;  DB 5;  Length 23;
  Best Local Similarity   70.6%;  Pred. No. 6.7e+03;
  Matches   12;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GGACCUGCCAGUGCUCU 19
              |||||:| ||| ||:|:
Db         19 GGACCTGACAGGGCTCT 3
```

RESULT 7
ACK21937/c
ID ACK21937 standard; DNA; 25 BP.
XX
AC ACK21937;
XX
DT 14-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 121918.
XX
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFFY-) AFFYMETRIX INC.
XX
PI Mittmann MP;
XX
DR WPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 121918; 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.goc/sequence.html
XX
SQ Sequence 25 BP; 5 A; 6 C; 7 G; 7 T; 0 U; 0 Other;

```
  Query Match             65.7%;  Score 13.8;  DB 9;  Length 25;
  Best Local Similarity   70.6%;  Pred. No. 6.8e+03;
  Matches   12;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 GACCUGCCAGUGCUCUT 20
              ||||:|||||  |:|:|
Db         21 GACCTGCCAGAACTCTT 5
```

RESULT 8
ACI58170/c
ID ACI58170 standard; DNA; 25 BP.
XX
AC ACI58170;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 58161.
XX
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.

XX
PA (APFY-) AFFYMETRIX INC.
XX
PI Mittmann MP;
XX
DR WPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 58161; 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.goc/sequence.html
XX
SQ Sequence 25 BP; 8 A; 6 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 65.7%; Score 13.8; DB 9; Length 25;
Best Local Similarity 70.6%; Pred. No. 6.8e+03;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 5 ACCUGCCAGUGCUCUTT 21
||| ||||| :| :|:||
Db 25 ACCAGCCAGTGTTCTTT 9

RESULT 9
ADC47044
ID ADC47044 standard; DNA; 29 BP.
XX
AC ADC47044;
XX
DT 18-DEC-2003 (first entry)
XX
DE BEC1 potassium channel inhibitor related primer #SEQ ID 6.
XX
KW BEC1 potassium channel inhibitor; nootropic; neuroprotective;
KW brain-specific eag-like channel 1; dementia; learning disability;
KW inhibitor; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO2003066099-A1.
XX
PD 14-AUG-2003.
XX
PF 03-FEB-2003; 2003WO-JP001065.
XX
PR 05-FEB-2002; 2002JP-00028844.
XX
PA (YAMA) YAMANOUCHI PHARM CO LTD.
XX
PI Kubota H, Suzuki T, Miura M, Nakai E, Yahiro K, Miyake A;
PI Mochizuki S, Nakatou K;
XX
DR WPI; 2003-697418/66.
XX
PT Antidementia agents comprise new and known brain-specific eag-like
PT channel 1 (BEC1) potassium channel inhibitors.
XX
PS Disclosure; Page 90; 95pp; Japanese.
XX
CC The invention relates to an antidementia agent that comprises a brain-
CC specific eag-like channel 1 (BEC1) potassium channel inhibitor. Agents of
CC the invention are used as BEC1 potassium channel inhibitors for treating
CC and preventing dementia and learning disabilities. The current sequence
CC represents the BEC1 potassium channel inhibitor related PCR primer
CC sequence.
XX
SQ Sequence 29 BP; 3 A; 11 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 65.7%; Score 13.8; DB 10; Length 29;
Best Local Similarity 70.6%; Pred. No. 6.9e+03;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GACCUGCCAGUGCUCUT 20
|||| ||| |:||:| |
Db 8 GACCTGCCCGTGCTCCT 24

RESULT 10
ADI35763
ID ADI35763 standard; DNA; 29 BP.
XX
AC ADI35763;
XX
DT 22-APR-2004 (first entry)
XX
DE Human potassium channel protein BEC1 related PCR primer SEQ ID NO:6.
XX
KW transgenic animal; potassium channel; BEC1; nootropic; tranquilliser;
KW dementia; memory loss; anxiety; learning ability; human; PCR; ss; primer.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2003041496-A1.
XX
PD 22-MAY-2003.
XX
PF 13-NOV-2002; 2002WO-JP011843.
XX
PR 14-NOV-2001; 2001JP-00349288.
XX
PA (YAMA) YAMANOUCHI PHARM CO LTD.
XX
PI Miyake A, Nakamura Y, Ni J, Mochizuki S;
XX
DR WPI; 2003-457459/43.
XX
PT Transgenic animal overexpressing potassium channel protein BEC1 for
PT screening potential treatments for dementia and anxiety.
XX
PS Example 1; SEQ ID NO 6; 56pp; Japanese.
XX
CC The present invention describes a transgenic animal transformed by a
CC promoter together with a polynucleotide encoding potassium channel
CC protein BEC1 or encoding a protein derived from BEC1 by addition,
CC deletion and/or substitution of up to ten amino acid residues and at
CC least 90% homologous to it. Also described: (1) screening (M1) for
CC substances for the treatment of dementia, memory loss and anxiety using
CC the transgenic animal as a disease model; and (2) the preparation (M2) of
CC drug compositions containing as active components substances identified
CC by (M1). BEC1 has nootropic and tranquilliser activities. The transgenic

```
CC   animal is useful as a disease model for in vivo screening of substances
CC   for the treatment and prevention of dementia, memory loss, and anxiety
CC   and for improving memory and learning ability. The present sequence
CC   represents a PCR primer for the human potassium channel protein BEC1,
CC   which is used in an example from the present invention.
XX
SQ   Sequence 29 BP; 3 A; 11 C; 9 G; 6 T; 0 U; 0 Other;

  Query Match             65.7%;  Score 13.8;  DB 10;  Length 29;
  Best Local Similarity   70.6%;  Pred. No. 6.9e+03;
  Matches   12;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 GACCUGCCAGUGCUCUT 20
              ||||:||| |:||:| |
Db          8 GACCTGCCCGTGCTCCT 24


RESULT 11
ABK67185/c
ID   ABK67185 standard; DNA; 26 BP.
XX
AC   ABK67185;
XX
DT   02-JUL-2002  (first entry)
XX
DE   Human gene specific PCR primer #1273.
XX
KW   Primer; ss; DNA microarray; differential expression analysis; human.
XX
OS   Homo sapiens.
XX
PN   US6352829-B1.
XX
PD   05-MAR-2002.
XX
PF   05-JAN-1999;   99US-00225928.
XX
PR   21-MAY-1997;   97US-00859998.
XX
PA   (CLON-) CLONTECH LAB INC.
XX
PI   Chenchik A,  Jokhadze G,  Bibilashvilli R;
XX
DR   WPI; 2002-314699/35.
XX
PT   Producing sub-population of labeled nucleic acids, useful for analyzing
PT   differences in RNA profiles between several different physiological
PT   sources, using set of distinct gene specific primers.
XX
PS   Example 3; SEQ ID NO 1273; 11pp; English.
XX
CC   The invention relates to producing a sub-population of labeled nucleic
CC   acids (NAs) comprising contacting a NA sample from a physiological
CC   source, with a pool of 50 distinct gene specific primers under suitable
CC   conditions to enzymatically generate sub-population of NAs, where each
CC   gene specific primer has a sequence complementary to a distinct mRNA, and
CC   each labeled NA is generated using a single gene specific primer. The
CC   method is useful for producing a sub-population of labeled NAs which is
CC   useful for analysing the differences in the RNA profiles between several
CC   different physiological sources, where the method comprises producing
CC   subpopulation of labeled NAs for the different physiological sources,
CC   comprising the populations for each physiological source to identify
CC   differences in the population, where the comparison is preferably
CC   performed by hybridising the labeled NAs for each of the distinct
CC   physiological sources to an array of probe NAs stably associated with the
CC   surface of a substrate to produce a hybridisation pattern for each of the
CC   sources, and comparing the patterns for each of the sources, where
CC   differential gene expression assays are utilised in differential
CC   expression analysis of diseased a normal tissue e.g. neoplastic a normal
CC   tissue, or different tissue or subtissue types. The present sequence is a
CC   human gene specific PCR primer used in the method of the invention. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from USPTO
CC   at http.wipo.seqdata.uspto.gov/sequence.html?DocID=6352829B1
XX
SQ   Sequence 26 BP; 11 A; 7 C; 7 G; 1 T; 0 U; 0 Other;

  Query Match             64.8%;  Score 13.6;  DB 6;  Length 26;
  Best Local Similarity   55.0%;  Pred. No. 8.5e+03;
  Matches   11;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 UAGGACCUGCCAGUGCUCUT 20
              : || | :||| |:||:|:|
Db         20 TTGGCCTTGCCGGTGCTCTT 1


RESULT 12
ABK67238
ID   ABK67238 standard; DNA; 26 BP.
XX
AC   ABK67238;
XX
DT   02-JUL-2002  (first entry)
XX
DE   Human gene specific PCR primer #1326.
XX
KW   Primer; ss; DNA microarray; differential expression analysis; human.
XX
OS   Homo sapiens.
XX
PN   US6352829-B1.
XX
PD   05-MAR-2002.
XX
PF   05-JAN-1999;   99US-00225928.
XX
PR   21-MAY-1997;   97US-00859998.
XX
PA   (CLON-) CLONTECH LAB INC.
XX
PI   Chenchik A,  Jokhadze G,  Bibilashvilli R;
XX
DR   WPI; 2002-314699/35.
XX
PT   Producing sub-population of labeled nucleic acids, useful for analyzing
PT   differences in RNA profiles between several different physiological
PT   sources, using set of distinct gene specific primers.
XX
PS   Example 3; SEQ ID NO 1326; 11pp; English.
XX
CC   The invention relates to producing a sub-population of labeled nucleic
CC   acids (NAs) comprising contacting a NA sample from a physiological
CC   source, with a pool of 50 distinct gene specific primers under suitable
CC   conditions to enzymatically generate sub-population of NAs, where each
CC   gene specific primer has a sequence complementary to a distinct mRNA, and
CC   each labeled NA is generated using a single gene specific primer. The
CC   method is useful for producing a sub-population of labeled NAs which is
CC   useful for analysing the differences in the RNA profiles between several
CC   different physiological sources, where the method comprises producing
CC   subpopulation of labeled NAs for the different physiological sources,
CC   comprising the populations for each physiological source to identify
CC   differences in the population, where the comparison is preferably
CC   performed by hybridising the labeled NAs for each of the distinct
CC   physiological sources to an array of probe NAs stably associated with the
CC   surface of a substrate to produce a hybridisation pattern for each of the
CC   sources, and comparing the patterns for each of the sources, where
CC   differential gene expression assays are utilised in differential
CC   expression analysis of diseased a normal tissue e.g. neoplastic a normal
CC   tissue, or different tissue or subtissue types. The present sequence is a
CC   human gene specific PCR primer used in the method of the invention. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from USPTO
CC   at http.wipo.seqdata.uspto.gov/sequence.html?DocID=6352829B1
XX
SQ   Sequence 26 BP; 5 A; 9 C; 5 G; 7 T; 0 U; 0 Other;
```

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  Query Match             64.8%;  Score 13.6;  DB 6;  Length 26;
  Best Local Similarity   65.0%;  Pred. No. 8.5e+03;
  Matches   13;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 AGGACCUGCCAGUGCUCUTT 21
              |||||| |||| |:  ||
Db          4 AGGACCTTCCAGTCCTACTT 23


RESULT 13
AAD51147
ID   AAD51147 standard; DNA; 28 BP.
XX
AC   AAD51147;
XX
DT   02-APR-2003  (first entry)
XX
DE   Adapter DNA #2 used to illustrate the method of the invention.
XX
KW   Genetic analysis; allelic analysis; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base    4
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "8-oxo-dG"
XX
PN   WO200279496-A2.
XX
PD   10-OCT-2002.
XX
PF   27-MAR-2002; 2002WO-US009928.
XX
PR   28-MAR-2001; 2001US-00821694.
XX
PA   (MIND-) APPLIED MINDS INC.
XX
PI   Hillis WD;
XX
DR   WPI; 2003-046825/04.
XX
PT   Obtaining information on target nucleic acid analyte, by hybridizing
PT   target with oligonucleotide probes complementary, or complementary except
PT   at position of interest to target and analyzing probe hybridization.
XX
PS   Example 1; Page 39; 66pp; English.
XX
CC   The invention relates to a method of obtaining information on a target
CC   nucleic acid analyte containing a target segment. The method involves
CC   hybridising target nucleic acid analyte with at least two oligonucleotide
CC   probes, where each probe comprises a sequence fully complementary, or
CC   complementary except at a position of interest or variable position, to
CC   the target nucleic acid analyte and analysing whether all, some or none
CC   of the probes hybridise. The method is useful for sequencing and for
CC   obtaining information on a number of target nucleic acid sequence
CC   segments, where information comprises the determination of a nucleotide
CC   at a position of interest. It is also useful for genetic or allelic
CC   analysis of genomic DNA or cDNA. The present sequence is an adapter DNA,
CC   used to illustrate the method of the invention
XX
SQ   Sequence 28 BP; 4 A; 7 C; 8 G; 6 T; 0 U; 3 Other;

  Query Match             64.8%;  Score 13.6;  DB 10;  Length 28;
  Best Local Similarity   65.0%;  Pred. No. 8.6e+03;
  Matches   13;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 AGGACCUGCCAGUGCUCUTT 21
              | || |:|||||: | |:||
Db          5 ACGAGCTGCCAGTCCGCTTT 24


RESULT 14
AAT32267
ID   AAT32267 standard; DNA; 25 BP.
XX
AC   AAT32267;
XX
DT   07-JAN-1997  (first entry)
XX
DE   Probe for the detection of lesions associated with neoplastic cells.
XX
KW   Probe; detection; lesion; neoplasia; neoplastic cells; cancer; prognosis;
KW   therapy; tumour cell; tumour; homozygous loss; ss.
XX
OS   Synthetic.
XX
PN   WO9619589-A1.
XX
PD   27-JUN-1996.
XX
PF   20-DEC-1995;   95WO-US016766.
XX
PR   20-DEC-1994;   94US-00360096.
XX
PA   (COLD-) COLD SPRING HARBOR LAB.
XX
PI   Wigler M,  Lisitsyn N;
XX
DR   WPI; 1996-309603/31.
XX
PT   Nucleic acid sequence probes - are used for the detection of lesions
PT   associated with neoplastic cells.
XX
PS   Claim 1; Page 23; 31pp; English.
XX
CC   The nucleic acid sequence probes described in AAT32244-78 are used for
CC   the detection of lesions associated with neoplastic cells. The sequences
CC   can be used for identifying the locus associated with the lesion, for
CC   determining cancer susceptibility of cells, as well as categorising and
CC   characterising tumour cells for prognosis and therapy. Two probes
CC   (AAT32267, AAT32268) were used to detect homozygous loss in tumour cell
CC   lines at chromosome location 18
XX
SQ   Sequence 25 BP; 5 A; 5 C; 8 G; 7 T; 0 U; 0 Other;

  Query Match             63.8%;  Score 13.4;  DB 2;  Length 25;
  Best Local Similarity   73.3%;  Pred. No. 1.1e+04;
  Matches   11;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 UAGGACCUGCCAGUG 15
              :|||| |:|||||:|
Db          3 TAGGAACTGCCAGTG 17


RESULT 15
AAT71677
ID   AAT71677 standard; DNA; 25 BP.
XX
AC   AAT71677;
XX
DT   04-FEB-1998  (first entry)
XX
DE   Cancer detection probe VAKO441-9 PCR 5' primer.
XX
KW   PCR primer; VAKO441-9; detection; neoplastic; lesion; tumour; RDA;
KW   homozygous loss; representational difference analysis; probe; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9722721-A2.
XX
PD   26-JUN-1997.
XX
```

PF 20-DEC-1996; 96WO-US020631.
XX
PR 21-DEC-1995; 95US-00576202.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
XX
PI Wigler M, Lisitsyn N;
XX
DR WPI; 1997-341709/31.
XX
PT New cancer detection probes - useful for detecting genomic lesions
PT associated with neoplasia in human cells, e.g. for detection, prognosis
PT and therapy of cancer.
XX
PS Claim 10; Page 23; 32pp; English.
XX
CC This primer is used to amplify a PCR product of 244 bp used as a probe in
CC a standard PCR panel for detemination of a lesion associated with
CC neoplasia in human cells. In particular, this probe identifies a
CC homozygous loss in tumour cell line at chromosome location 18. The DNA
CC can be obtained by standard representational difference analysis (RDA).
CC RDA was performed using Bgl II restriction endonuclease on tumour DNA
CC (driver) and matched with normal DNA (tester). Pure tumour DNAs of the
CC RDA difference products were cloned into plasmids. Selected plasmid
CC inserts were analysed by Southern blot hybridisation. Oligonucleotides
CC synthesised from selected plasmid insert sequences were used to screen a
CC standard PCR panel of DNAs from tumour cell lines and a control DNA.
CC Probes were subsequently mapped to human chromosomes by PCR using an
CC existing panel of human, rodent somatic cell hybrids. The DNA can be used
CC for detecting genomic lesions associated with cancer and for prognosis
CC and therapy. The DNA sequences can also be used to obtain other suitable
CC probes by walking genomic DNA to obtain a asecondary probe, and repeating
CC the walking to obtain successive probes which are screened with normal
CC and tumour cells
XX
SQ Sequence 25 BP; 5 A; 5 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 63.8%; Score 13.4; DB 2; Length 25;
Best Local Similarity 73.3%; Pred. No. 1.1e+04;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 UAGGACCUGCCAGUG 15
              :|||| |:|||||:|
Db          3 TAGGAACTGCCAGTG 17
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Search completed: September 30, 2005, 09:14:08
Job time : 421 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 30, 2005, 09:06:54 ; Search time 123 Seconds
(without alignments)
279.364 Million cell updates/sec

Title: US-10-738-413-1
Perfect score: 21
Sequence: 1 uaggaccugccagugcucutt 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 569154

Minimum DB seq length: 21
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	15.8	75.2	25	4	US-09-396-196G-107545	Sequence 107545,
	2	14.8	70.5	25	4	US-09-396-196G-40269	Sequence 40269, A
	3	14.8	70.5	25	4	US-09-396-196G-55195	Sequence 55195, A
	4	14.8	70.5	25	4	US-09-396-196G-55196	Sequence 55196, A
	5	14.4	68.6	25	4	US-09-396-196G-48277	Sequence 48277, A
	6	14.4	68.6	25	4	US-09-396-196G-107546	Sequence 107546,
	7	14	66.7	25	4	US-09-396-196G-48278	Sequence 48278, A
c	8	14	66.7	25	4	US-09-396-196G-52121	Sequence 52121, A
c	9	14	66.7	25	4	US-09-396-196G-52122	Sequence 52122, A
c	10	13.6	64.8	26	2	US-08-859-998-1273	Sequence 1273, Ap
	11	13.6	64.8	26	2	US-08-859-998-1326	Sequence 1326, Ap
c	12	13.6	64.8	26	3	US-09-225-928-1273	Sequence 1273, Ap
	13	13.6	64.8	26	3	US-09-225-928-1326	Sequence 1326, Ap
c	14	13.6	64.8	26	4	US-09-225-201B-1273	Sequence 1273, Ap
	15	13.6	64.8	26	4	US-09-225-201B-1326	Sequence 1326, Ap
c	16	13.4	63.8	23	4	US-09-873-737A-12	Sequence 12, Appl
	17	13.4	63.8	25	1	US-08-360-096-15	Sequence 15, Appl
	18	13.4	63.8	25	3	US-08-576-202-24	Sequence 24, Appl
	19	13.4	63.8	25	4	US-09-396-196G-48276	Sequence 48276, A
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	22	13.4	63.8	25	5	PCT-US95-16766-24	Sequence 24, Appl
	23	13.2	62.9	25	4	US-09-396-196G-18422	Sequence 18422, A
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	25	13.2	62.9	25	4	US-09-396-196G-66672	Sequence 66672, A
	26	13.2	62.9	25	4	US-09-396-196G-66673	Sequence 66673, A
	27	13.2	62.9	25	4	US-09-396-196G-66674	Sequence 66674, A
	28	13.2	62.9	25	4	US-09-396-196G-122627	Sequence 122627,
	29	13	61.9	25	4	US-09-396-196G-107084	Sequence 107084,
c	30	12.8	61.0	25	4	US-09-396-196G-5116	Sequence 5116, Ap
	31	12.8	61.0	25	4	US-09-396-196G-62374	Sequence 62374, A
	32	12.8	61.0	25	4	US-09-396-196G-68909	Sequence 68909, A
	33	12.8	61.0	25	4	US-09-396-196G-81723	Sequence 81723, A
	34	12.8	61.0	25	4	US-09-396-196G-107544	Sequence 107544,
c	35	12.6	60.0	25	4	US-09-396-196G-14106	Sequence 14106, A
	36	12.6	60.0	25	4	US-09-396-196G-64352	Sequence 64352, A
	37	12.6	60.0	25	4	US-09-396-196G-64353	Sequence 64353, A
c	38	12.6	60.0	25	4	US-09-396-196G-91219	Sequence 91219, A
c	39	12.6	60.0	25	4	US-09-396-196G-91220	Sequence 91220, A
	40	12.6	60.0	25	4	US-09-396-196G-93099	Sequence 93099, A
	41	12.6	60.0	25	4	US-09-396-196G-113638	Sequence 113638,
	42	12.6	60.0	25	4	US-09-396-196G-113639	Sequence 113639,
c	43	12.6	60.0	30	2	US-08-859-998-1260	Sequence 1260, Ap
c	44	12.6	60.0	30	3	US-09-225-928-1260	Sequence 1260, Ap
c	45	12.6	60.0	30	4	US-09-225-201B-1260	Sequence 1260, Ap

ALIGNMENTS

RESULT 1
US-09-396-196G-107545
; Sequence 107545, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 107545
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-107545

Query Match 75.2%; Score 15.8; DB 4; Length 25;
Best Local Similarity 68.4%; Pred. No. 1.9e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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Qy          2 AGGACCUGCCAGUGCUCUT 20
              | || |:|||||:||:|:|
Db          1 AAGAGCTGCCAGTGCTCTT 19
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RESULT 2
US-09-396-196G-40269
; Sequence 40269, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40269

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;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-396-196G-40269

  Query Match            70.5%;  Score 14.8;  DB 4;  Length 25;
  Best Local Similarity   66.7%;  Pred. No. 5.9e+02;
  Matches   12;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 UAGGACCUGCCAGUGCUC 18
              :|||| |:|||||:| :|
Db          2 TAGGAACTGCCAGTGTTC 19


RESULT 3
US-09-396-196G-55195
; Sequence 55195, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196G
;  CURRENT FILING DATE:  1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 55195
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
US-09-396-196G-55195

  Query Match            70.5%;  Score 14.8;  DB 4;  Length 25;
  Best Local Similarity   66.7%;  Pred. No. 5.9e+02;
  Matches   12;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 GACCUGCCAGUGCUCUTT 21
              || |:||| |:||:|:||
Db          7 GAGCTGCCTGTGCTCTTT 24


RESULT 4
US-09-396-196G-55196
; Sequence 55196, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196G
;  CURRENT FILING DATE:  1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 55196
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
US-09-396-196G-55196

  Query Match            70.5%;  Score 14.8;  DB 4;  Length 25;
  Best Local Similarity   66.7%;  Pred. No. 5.9e+02;
  Matches   12;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 GACCUGCCAGUGCUCUTT 21
              || |:||| |:||:|:||
Db          1 GAGCTGCCTGTGCTCTTT 18


RESULT 5
US-09-396-196G-48277
; Sequence 48277, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196G
;  CURRENT FILING DATE:  1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48277
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
US-09-396-196G-48277

  Query Match            68.6%;  Score 14.4;  DB 4;  Length 25;
  Best Local Similarity   68.8%;  Pred. No. 9.2e+02;
  Matches   11;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 ACCUGCCAGUGCUCUT 20
              | |:|||||:||:|:|
Db          2 AACTGCCAGTGCTCTT 17


RESULT 6
US-09-396-196G-107546
; Sequence 107546, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196G
;  CURRENT FILING DATE:  1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 107546
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
US-09-396-196G-107546

  Query Match            68.6%;  Score 14.4;  DB 4;  Length 25;
  Best Local Similarity   68.8%;  Pred. No. 9.2e+02;
  Matches   11;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 ACCUGCCAGUGCUCUT 20
              | |:|||||:||:|:|
Db          1 AGCTGCCAGTGCTCTT 16


RESULT 7
US-09-396-196G-48278
; Sequence 48278, Application US/09396196G
; Patent No. 6821724
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; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196G
;  CURRENT FILING DATE:  1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48278
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
US-09-396-196G-48278

  Query Match             66.7%;  Score 14;  DB 4;  Length 25;
  Best Local Similarity   71.4%;  Pred. No. 1.4e+03;
  Matches   10;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CUGCCAGUGCUCUT 20
              |:|||||:||:|:|
Db          1 CTGCCAGTGCTCTT 14


RESULT 8
US-09-396-196G-52121/c
; Sequence 52121, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196G
;  CURRENT FILING DATE:  1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52121
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
US-09-396-196G-52121

  Query Match             66.7%;  Score 14;  DB 4;  Length 25;
  Best Local Similarity   71.4%;  Pred. No. 1.4e+03;
  Matches   10;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CUGCCAGUGCUCUT 20
              |:|||||:||:|:|
Db         21 CTGCCAGTGCTCTT 8


RESULT 9
US-09-396-196G-52122/c
; Sequence 52122, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196G
;  CURRENT FILING DATE:  1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52122
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
US-09-396-196G-52122

  Query Match             66.7%;  Score 14;  DB 4;  Length 25;
  Best Local Similarity   71.4%;  Pred. No. 1.4e+03;
  Matches   10;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CUGCCAGUGCUCUT 20
              |:|||||:||:|:|
Db         18 CTGCCAGTGCTCTT 5


RESULT 10
US-08-859-998-1273/c
; Sequence 1273, Application US/08859998
; Patent No. 5994076
;  GENERAL INFORMATION:
;    APPLICANT:  Chenchik, Alex
;    APPLICANT:  Jokhadze, George
;    APPLICANT:  Bibilashvilli, Robert
;    TITLE OF INVENTION:  METHOD OF ASSAYING DIFFERENTIAL
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1375
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  2200 Sand Hill Road, Suite 100
;      CITY:  Menlo Park
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,998
;      FILING DATE:  21-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Field, Bret E.
;      REGISTRATION NUMBER:  37,620
;      REFERENCE/DOCKET NUMBER:  09096/002001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-322-5070
;      TELEFAX:  415-854-0875
;  INFORMATION FOR SEQ ID NO:  1273:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      OTHER INFORMATION:  oligonucleotide primer
US-08-859-998-1273

  Query Match             64.8%;  Score 13.6;  DB 2;  Length 26;
  Best Local Similarity   55.0%;  Pred. No. 2.3e+03;
  Matches   11;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 UAGGACCUGCCAGUGCUCUT 20
              : || | :||| |:||:|:|
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Db         20 TTGGCCTTGCCGGTGCTCTT 1


RESULT 11
US-08-859-998-1326
; Sequence 1326, Application US/08859998
; Patent No. 5994076
;  GENERAL INFORMATION:
;    APPLICANT:  Chenchik, Alex
;    APPLICANT:  Jokhadze, George
;    APPLICANT:  Bibilashvilli, Robert
;    TITLE OF INVENTION:  METHOD OF ASSAYING DIFFERENTIAL
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1375
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  2200 Sand Hill Road, Suite 100
;      CITY:  Menlo Park
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,998
;      FILING DATE:  21-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Field, Bret E.
;      REGISTRATION NUMBER:  37,620
;      REFERENCE/DOCKET NUMBER:  09096/002001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-322-5070
;      TELEFAX:  415-854-0875
;  INFORMATION FOR SEQ ID NO:  1326:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      OTHER INFORMATION:  oligonucleotide primer
US-08-859-998-1326

  Query Match             64.8%;  Score 13.6;  DB 2;  Length 26;
  Best Local Similarity   65.0%;  Pred. No. 2.3e+03;
  Matches   13;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 AGGACCUGCCAGUGCUCUTT 21
              ||||||: ||||: |:  ||
Db          4 AGGACCTTCCAGTCCTACTT 23


RESULT 12
US-09-225-928-1273/c
; Sequence 1273, Application US/09225928
; Patent No. 6352829
;  GENERAL INFORMATION:
;       APPLICANT: Chenchik, Alex
;                  Jokhadze, George
;                  Bibilashvilli, Robert
;       TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;                           EXPRESSION
;       NUMBER OF SEQUENCES: 1375
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Fish & Richardson, P.C.
;            STREET: 2200 Sand Hill Road, Suite 100
;            CITY: Menlo Park
;            STATE: CA
;            COUNTRY: US
;            ZIP: 94025
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: Windows95
;            SOFTWARE: FastSEQ for Windows Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/225,928
;            FILING DATE: 05-Jan-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/859,998
;            FILING DATE: 21-MAY-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Field, Bret E.
;            REGISTRATION NUMBER: 37,620
;            REFERENCE/DOCKET NUMBER: 09096/002001
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 415-322-5070
;            TELEFAX: 415-854-0875
;  INFORMATION FOR SEQ ID NO: 1273:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 26 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       FEATURE:
;            OTHER INFORMATION:  oligonucleotide primer
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1273:
US-09-225-928-1273

  Query Match             64.8%;  Score 13.6;  DB 3;  Length 26;
  Best Local Similarity   55.0%;  Pred. No. 2.3e+03;
  Matches   11;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 UAGGACCUGCCAGUGCUCUT 20
              : || | :||| |:||:|:|
Db         20 TTGGCCTTGCCGGTGCTCTT 1


RESULT 13
US-09-225-928-1326
; Sequence 1326, Application US/09225928
; Patent No. 6352829
;  GENERAL INFORMATION:
;       APPLICANT: Chenchik, Alex
;                  Jokhadze, George
;                  Bibilashvilli, Robert
;       TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;                           EXPRESSION
;       NUMBER OF SEQUENCES: 1375
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Fish & Richardson, P.C.
;            STREET: 2200 Sand Hill Road, Suite 100
;            CITY: Menlo Park
;            STATE: CA
;            COUNTRY: US
;            ZIP: 94025
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: Windows95
;            SOFTWARE: FastSEQ for Windows Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/225,928
;            FILING DATE: 05-Jan-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
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;             APPLICATION NUMBER: 08/859,998
;             FILING DATE: 21-MAY-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Field, Bret E.
;             REGISTRATION NUMBER: 37,620
;             REFERENCE/DOCKET NUMBER: 09096/002001
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415-322-5070
;             TELEFAX: 415-854-0875
;   INFORMATION FOR SEQ ID NO: 1326:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 26 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             OTHER INFORMATION:  oligonucleotide primer
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1326:
US-09-225-928-1326

  Query Match             64.8%;  Score 13.6;  DB 3;  Length 26;
  Best Local Similarity   65.0%;  Pred. No. 2.3e+03;
  Matches   13;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 AGGACCUGCCAGUGCUCUTT 21
              |||||| |||| |:  ||
Db          4 AGGACCTTCCAGTCCTACTT 23


RESULT 14
US-09-225-201B-1273/c
; Sequence 1273, Application US/09225201B
; Patent No. 6489455
;   GENERAL INFORMATION:
;        APPLICANT: Chenchik, Alex
;                   Jokhadze, George
;                   Bibilashvilli, Robert
;        TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;                            EXPRESSION
;        NUMBER OF SEQUENCES: 1375
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Fish & Richardson, P.C.
;             STREET: 2200 Sand Hill Road, Suite 100
;             CITY: Menlo Park
;             STATE: CA
;             COUNTRY: US
;             ZIP: 94025
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: Windows95
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/225,201B
;             FILING DATE: 05-Jan-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/859,998
;             FILING DATE: 21-MAY-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Field, Bret E.
;             REGISTRATION NUMBER: 37,620
;             REFERENCE/DOCKET NUMBER: 09096/002001
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415-322-5070
;             TELEFAX: 415-854-0875
;   INFORMATION FOR SEQ ID NO: 1273:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 26 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             OTHER INFORMATION:  oligonucleotide primer
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1273:
US-09-225-201B-1273

  Query Match             64.8%;  Score 13.6;  DB 4;  Length 26;
  Best Local Similarity   55.0%;  Pred. No. 2.3e+03;
  Matches   11;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 UAGGACCUGCCAGUGCUCUT 20
              : || | :||| |:||:|:|
Db         20 TTGGCCTTGCCGGTGCTCTT 1


RESULT 15
US-09-225-201B-1326
; Sequence 1326, Application US/09225201B
; Patent No. 6489455
;   GENERAL INFORMATION:
;        APPLICANT: Chenchik, Alex
;                   Jokhadze, George
;                   Bibilashvilli, Robert
;        TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;                            EXPRESSION
;        NUMBER OF SEQUENCES: 1375
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Fish & Richardson, P.C.
;             STREET: 2200 Sand Hill Road, Suite 100
;             CITY: Menlo Park
;             STATE: CA
;             COUNTRY: US
;             ZIP: 94025
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: Windows95
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/225,201B
;             FILING DATE: 05-Jan-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/859,998
;             FILING DATE: 21-MAY-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Field, Bret E.
;             REGISTRATION NUMBER: 37,620
;             REFERENCE/DOCKET NUMBER: 09096/002001
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415-322-5070
;             TELEFAX: 415-854-0875
;   INFORMATION FOR SEQ ID NO: 1326:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 26 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             OTHER INFORMATION:  oligonucleotide primer
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1326:
US-09-225-201B-1326

  Query Match             64.8%;  Score 13.6;  DB 4;  Length 26;
  Best Local Similarity   65.0%;  Pred. No. 2.3e+03;
  Matches   13;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 AGGACCUGCCAGUGCUCUTT 21
              |||||| |||| |:  ||
Db          4 AGGACCTTCCAGTCCTACTT 23
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OM nucleic - nucleic search, using sw model

Run on: September 30, 2005, 09:06:54 ; Search time 3585 Seconds
(without alignments)
40.446 Million cell updates/sec

Title: US-10-738-413-1
Perfect score: 21
Sequence: 1 uaggaccugccagugcucutt 21

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Gapop 10.0 , Gapext 1.0

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Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	3	15.2	72.4	25	21	US-10-719-900-424586	Sequence 424586,
	4	14.8	70.5	25	21	US-10-809-189-40269	Sequence 40269, A
	5	14.8	70.5	25	21	US-10-809-189-55195	Sequence 55195, A
	6	14.8	70.5	25	21	US-10-809-189-55196	Sequence 55196, A
	7	14.8	70.5	25	21	US-10-956-157-154607	Sequence 154607,
	8	14.8	70.5	25	22	US-10-719-956-560046	Sequence 560046,
	9	14.8	70.5	25	22	US-10-719-956-560047	Sequence 560047,
	10	14.6	69.5	28	17	US-10-407-089-5	Sequence 5, Appli
	11	14.4	68.6	25	21	US-10-719-900-355242	Sequence 355242,
c	12	14.4	68.6	25	21	US-10-719-900-726466	Sequence 726466,
c	13	14.4	68.6	25	21	US-10-719-900-867852	Sequence 867852,
	14	14.4	68.6	25	21	US-10-719-900-961525	Sequence 961525,
	15	14.4	68.6	25	21	US-10-809-189-48277	Sequence 48277, A
	16	14.4	68.6	25	21	US-10-809-189-107546	Sequence 107546,
c	17	14.4	68.6	25	22	US-10-719-956-35641	Sequence 35641, A
c	18	14.4	68.6	25	22	US-10-719-956-124951	Sequence 124951,
	19	14.4	68.6	25	22	US-10-719-956-475343	Sequence 475343,
c	20	14.2	67.6	25	15	US-10-098-263B-63689	Sequence 63689, A
c	21	14.2	67.6	25	21	US-10-719-900-59543	Sequence 59543, A
	22	14.2	67.6	25	21	US-10-719-900-145845	Sequence 145845,
c	23	14.2	67.6	25	21	US-10-719-900-436263	Sequence 436263,
	24	14.2	67.6	25	21	US-10-719-900-477557	Sequence 477557,
	25	14.2	67.6	25	21	US-10-719-900-485539	Sequence 485539,
c	26	14.2	67.6	25	21	US-10-719-900-787669	Sequence 787669,
	27	14.2	67.6	25	22	US-10-719-956-34410	Sequence 34410, A
	28	14.2	67.6	25	22	US-10-719-956-44564	Sequence 44564, A
	29	14.2	67.6	25	22	US-10-719-956-139996	Sequence 139996,
	30	14.2	67.6	25	22	US-10-719-956-152482	Sequence 152482,
	31	14.2	67.6	25	22	US-10-719-956-156015	Sequence 156015,
c	32	14.2	67.6	25	22	US-10-719-956-556350	Sequence 556350,
	33	14.2	67.6	28	10	US-09-821-694A-16	Sequence 16, Appl
	34	14.2	67.6	28	11	US-09-821-694A-16	Sequence 16, Appl
	35	14.2	67.6	30	22	US-10-723-681-321	Sequence 321, App
	36	14	66.7	25	21	US-10-719-900-455910	Sequence 455910,
c	37	14	66.7	25	21	US-10-719-900-589497	Sequence 589497,
	38	14	66.7	25	21	US-10-719-900-655445	Sequence 655445,
	39	14	66.7	25	21	US-10-809-189-48278	Sequence 48278, A
c	40	14	66.7	25	21	US-10-809-189-52121	Sequence 52121, A
c	41	14	66.7	25	21	US-10-809-189-52122	Sequence 52122, A
c	42	13.8	65.7	25	15	US-10-098-263B-58161	Sequence 58161, A
c	43	13.8	65.7	25	15	US-10-098-263B-121918	Sequence 121918,
	44	13.8	65.7	25	21	US-10-719-900-58044	Sequence 58044, A
	45	13.8	65.7	25	21	US-10-719-900-118070	Sequence 118070,

ALIGNMENTS

RESULT 1
US-10-738-413-1
; Sequence 1, Application US/10738413
; Publication No. US20050137151A1
; GENERAL INFORMATION:
; APPLICANT: BINETTI, RALPH R.
; APPLICANT: JONES, BRIAN C.
; TITLE OF INVENTION: SI-RNA-MEDIATED GENE SILENCING TECHNOLOGY TO INHIBIT
; TITLE OF INVENTION: TYROSINASE AND REDUCE PIGMENTATION
; FILE REFERENCE: SC66U-US
; CURRENT APPLICATION NUMBER: US/10/738,413
; CURRENT FILING DATE: 2003-12-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-738-413-1

Query Match 100.0%; Score 21; DB 22; Length 21;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 UAGGACCUGCCAGUGCUCUTT 21
              ||||||||||||||||||||
Db          1 UAGGACCUGCCAGUGCUCUTT 21


RESULT 2
US-10-809-189-107545
; Sequence 107545, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/10/809,189
;  CURRENT FILING DATE:  2004-03-25
;  PRIOR APPLICATION NUMBER: US/09/396,196
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 107545
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
US-10-809-189-107545

  Query Match             75.2%;  Score 15.8;  DB 21;  Length 25;
  Best Local Similarity   68.4%;  Pred. No. 4.6e+02;
  Matches   13;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 AGGACCUGCCAGUGCUCUT 20
              | ||  |:|||||:||:|:|
Db          1 AAGAGCTGCCAGTGCTCTT 19


RESULT 3
US-10-719-900-424586/c
; Sequence 424586, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528.1
;  CURRENT APPLICATION NUMBER: US/10/719,900
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,808
;  PRIOR FILING DATE: 2002 11 20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 424586
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-719-900-424586

  Query Match             72.4%;  Score 15.2;  DB 21;  Length 25;
  Best Local Similarity   60.0%;  Pred. No. 9.4e+02;
  Matches   12;  Conservative    5;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 UAGGACCUGCCAGUGCUCUT 20
              : |||||:|||||:  :|:|
Db         21 TTGGACCTGCCAGTAATCTT 2


RESULT 4
US-10-809-189-40269
; Sequence 40269, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/10/809,189
;  CURRENT FILING DATE:  2004-03-25
;  PRIOR APPLICATION NUMBER: US/09/396,196
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40269
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-809-189-40269

  Query Match             70.5%;  Score 14.8;  DB 21;  Length 25;
  Best Local Similarity   66.7%;  Pred. No. 1.5e+03;
  Matches   12;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 UAGGACCUGCCAGUGCUC 18
              :|||| |:|||||:| :|
Db          2 TAGGAACTGCCAGTGTTC 19


RESULT 5
US-10-809-189-55195
; Sequence 55195, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/10/809,189
;  CURRENT FILING DATE:  2004-03-25
;  PRIOR APPLICATION NUMBER: US/09/396,196
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 55195
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
US-10-809-189-55195

  Query Match             70.5%;  Score 14.8;  DB 21;  Length 25;
  Best Local Similarity   66.7%;  Pred. No. 1.5e+03;
  Matches   12;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 GACCUGCCAGUGCUCUTT 21
              || |:||| |:||:|:||
Db          7 GAGCTGCCTGTGCTCTTT 24


RESULT 6
US-10-809-189-55196
; Sequence 55196, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
```

```
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/10/809,189
;  CURRENT FILING DATE:  2004-03-25
;  PRIOR APPLICATION NUMBER: US/09/396,196
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 55196
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
US-10-809-189-55196

  Query Match             70.5%;  Score 14.8;  DB 21;  Length 25;
  Best Local Similarity   66.7%;  Pred. No. 1.5e+03;
  Matches   12;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 GACCUGCCAGUGCUCUTT 21
              || |:||| |:||:|:||
Db          1 GAGCTGCCTGTGCTCTTT 18


RESULT 7
US-10-956-157-154607
; Sequence 154607, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William
;  TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
;  TITLE OF INVENTION:  HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
;  FILE REFERENCE: 031896-043000 (AM 101081)
;  CURRENT APPLICATION NUMBER: US/10/956,157
;  CURRENT FILING DATE:  2004-10-04
;  NUMBER OF SEQ ID NOS: 319805
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 154607
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Probe Sequence
US-10-956-157-154607

  Query Match             70.5%;  Score 14.8;  DB 21;  Length 25;
  Best Local Similarity   66.7%;  Pred. No. 1.5e+03;
  Matches   12;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 AGGACCUGCCAGUGCUCU 19
              |||| |:| |||:||:|:
Db          4 AGGATCTGACAGTGCTCT 21


RESULT 8
US-10-719-956-560046
; Sequence 560046, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Rat
;  FILE REFERENCE: 3527.1
;  CURRENT APPLICATION NUMBER: US/10/719,956
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,836
;  PRIOR FILING DATE: 2002 11 20
;  NUMBER OF SEQ ID NOS: 699466
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 560046
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-10-719-956-560046

  Query Match             70.5%;  Score 14.8;  DB 22;  Length 25;
  Best Local Similarity   66.7%;  Pred. No. 1.5e+03;
  Matches   12;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 UAGGACCUGCCAGUGCUC 18
              :||||||:| || :||:|
Db          1 TAGGACCTGACAATGCTC 18


RESULT 9
US-10-719-956-560047
; Sequence 560047, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Rat
;  FILE REFERENCE: 3527.1
;  CURRENT APPLICATION NUMBER: US/10/719,956
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,836
;  PRIOR FILING DATE: 2002 11 20
;  NUMBER OF SEQ ID NOS: 699466
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 560047
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-10-719-956-560047

  Query Match             70.5%;  Score 14.8;  DB 22;  Length 25;
  Best Local Similarity   66.7%;  Pred. No. 1.5e+03;
  Matches   12;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 UAGGACCUGCCAGUGCUC 18
              :||||||:| || :||:|
Db          1 TAGGACCTGACATTGCTC 18


RESULT 10
US-10-407-089-5
; Sequence 5, Application US/10407089
; Publication No. US20030224419A1
; GENERAL INFORMATION:
;  APPLICANT: Corcoran, Kevin C.
;  APPLICANT:  Eletr, Sam
;  TITLE OF INVENTION: System for Determining a Signature of a
;  TITLE OF INVENTION:  Nucleotide Sequence
;  FILE REFERENCE: 55525-8040.US00
;  CURRENT APPLICATION NUMBER: US/10/407,089
;  CURRENT FILING DATE:  2003-04-02
;  PRIOR APPLICATION NUMBER: US/09/654,187
;  PRIOR FILING DATE: 2000-09-01
;  PRIOR APPLICATION NUMBER: US 60/182,454
;  PRIOR FILING DATE: 2000-02-15
;  PRIOR APPLICATION NUMBER: PCT/US98/11224
;  PRIOR FILING DATE: 1998-05-22
;  PRIOR APPLICATION NUMBER: US 08/862,610
;  PRIOR FILING DATE: 1997-05-23
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 28
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: encoded adaptor
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(28)
;   OTHER INFORMATION: n = A,T,C or G
US-10-407-089-5

  Query Match             69.5%;  Score 14.6;  DB 17;  Length 28;
```

```
  Best Local Similarity   61.9%;  Pred. No. 1.9e+03;
  Matches   13;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 UAGGACCUGCCAGUGCUCUTT 21
              :| || |:|||||: | |:||
Db          4 TACGAGCTGCCAGTCCGCTTT 24


RESULT 11
US-10-719-900-355242
; Sequence 355242, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528.1
;  CURRENT APPLICATION NUMBER: US/10/719,900
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,808
;  PRIOR FILING DATE: 2002 11 20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 355242
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-719-900-355242

  Query Match             68.6%;  Score 14.4;  DB 21;  Length 25;
  Best Local Similarity   68.8%;  Pred. No. 2.4e+03;
  Matches   11;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CCUGCCAGUGCUCUTT 21
              ||:|||||: |:|:||
Db          1 CCTGCCAGTCCTCTTT 16


RESULT 12
US-10-719-900-726466/c
; Sequence 726466, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528.1
;  CURRENT APPLICATION NUMBER: US/10/719,900
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,808
;  PRIOR FILING DATE: 2002 11 20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 726466
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-719-900-726466

  Query Match             68.6%;  Score 14.4;  DB 21;  Length 25;
  Best Local Similarity   75.0%;  Pred. No. 2.4e+03;
  Matches   12;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AGGACCUGCCAGUGCU 17
              || |||:|||||:||:
Db         25 AGTACCTGCCAGTGCT 10


RESULT 13
US-10-719-900-867852/c
; Sequence 867852, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528.1
;  CURRENT APPLICATION NUMBER: US/10/719,900
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,808
;  PRIOR FILING DATE: 2002 11 20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 867852
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-719-900-867852

  Query Match             68.6%;  Score 14.4;  DB 21;  Length 25;
  Best Local Similarity   81.2%;  Pred. No. 2.4e+03;
  Matches   13;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 UAGGACCUGCCAGUGC 16
              :||||||:||||| ||
Db         17 TAGGACCTGCCAGGGC 2


RESULT 14
US-10-719-900-961525
; Sequence 961525, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528.1
;  CURRENT APPLICATION NUMBER: US/10/719,900
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,808
;  PRIOR FILING DATE: 2002 11 20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 961525
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-719-900-961525

  Query Match             68.6%;  Score 14.4;  DB 21;  Length 25;
  Best Local Similarity   75.0%;  Pred. No. 2.4e+03;
  Matches   12;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AGGACCUGCCAGUGCU 17
              |||| |:|||||:||:
Db          8 AGGAGCTGCCAGTGCT 23


RESULT 15
US-10-809-189-48277
; Sequence 48277, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/10/809,189
;  CURRENT FILING DATE:  2004-03-25
;  PRIOR APPLICATION NUMBER: US/09/396,196
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48277
;   LENGTH: 25
;   TYPE: DNA
```

```
;   ORGANISM: mus musculus
US-10-809-189-48277

  Query Match             68.6%;  Score 14.4;  DB 21;  Length 25;
  Best Local Similarity   68.8%;  Pred. No. 2.4e+03;
  Matches   11;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 ACCUGCCAGUGCUCUT 20
              | |:|||||:||:|:|
Db          2 AACTGCCAGTGCTCTT 17


Search completed: September 30, 2005, 10:13:59
Job time : 3585 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 30, 2005, 09:06:54 ; Search time 2985 Seconds
(without alignments)
267.789 Million cell updates/sec

Title: US-10-738-413-1
Perfect score: 21
Sequence: 1 uaggaccugccagugcucutt 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 34436

Minimum DB seq length: 21
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	12.6	60.0	30	9	CL982942	GC0170 TI
	2	12.2	58.1	28	8	AZ821702	AZ821702 2M0094O01
	3	12.2	58.1	28	9	AG192441	AG192441 Pan trogl
c	4	11.6	55.2	28	1	AI370776	AI370776 qz89c10.x
	5	11	52.4	22	9	AJ592231	AJ592231 Arabidops
	6	11	52.4	29	8	AZ847949	AZ847949 2M0148B23
c	7	10.8	51.4	26	8	AZ815857	AZ815857 2M0084A01
c	8	10.6	50.5	24	8	AZ617463	AZ617463 1M0448F15
	9	10.4	49.5	28	1	AL042578	AL042578 DKFZp434J
	10	10.4	49.5	28	8	AZ642513	AZ642513 1M0505N01
c	11	10.4	49.5	29	8	AZ454477	AZ454477 1M0256N22
c	12	10.4	49.5	30	4	BG424013	BG424013 602447475
c	13	10.2	48.6	22	8	AZ603158	AZ603158 1M0422L13
c	14	10.2	48.6	28	1	AA937308	AA937308 om16h06.s
	15	10.2	48.6	28	9	AB004341	AB004341 Mouse gen
	16	10.2	48.6	29	8	AZ315608	AZ315608 1M0032G23
c	17	10.2	48.6	29	8	AZ618039	AZ618039 1M0449O04
c	18	10.2	48.6	29	8	AZ663335	AZ663335 1M0542J20
c	19	10	47.6	22	8	AZ324102	AZ324102 1M0045H23
c	20	10	47.6	22	8	AZ345644	AZ345644 1M0080J22
	21	10	47.6	23	9	TA70C10Q	AL458148 T. brucei
	22	10	47.6	24	9	CL666753	CL666753 PRI0153b_
c	23	10	47.6	25	9	TA257D02Q	AL481946 T. brucei
c	24	10	47.6	26	1	AJ747615	AJ747615 AJ747615
c	25	10	47.6	26	9	CG721091	CG721091 1119065D0
c	26	10	47.6	27	8	AZ329457	AZ329457 1M0053P08
c	27	10	47.6	27	9	CG723351	CG723351 1119076A0
	28	10	47.6	29	7	CF292082	CF292082 14ROOT--0
	29	10	47.6	29	7	CF295445	CF295445 30DGS--05
	30	10	47.6	29	7	CF295451	CF295451 30DGS--05
c	31	10	47.6	30	4	BM392665	BM392665 50071-2-1
c	32	10	47.6	30	4	BM393859	BM393859 50072-2-1
c	33	9.8	46.7	22	1	AI153141	AI153141 ud55a10.r
	34	9.8	46.7	23	8	AZ810074	AZ810074 2M0074J19
c	35	9.8	46.7	23	8	AZ810074	AZ810074 2M0074J19
	36	9.8	46.7	24	8	AZ588136	AZ588136 1M0396E09
	37	9.8	46.7	25	8	AZ634204	AZ634204 1M0489C24
	38	9.8	46.7	25	8	AZ807605	AZ807605 2M0070L05
c	39	9.8	46.7	25	9	AG188322	AG188322 Pan trogl
c	40	9.8	46.7	26	9	TA30H08Q	AL452912 T. brucei
c	41	9.8	46.7	26	9	CL438164	CL438164 PST6934-N
	42	9.8	46.7	27	8	AZ489568	AZ489568 1M0322P04
	43	9.8	46.7	28	8	AZ641309	AZ641309 1M0503G17
	44	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
	45	9.8	46.7	29	8	AZ766277	AZ766277 1M0563A15

ALIGNMENTS

RESULT 1
CL982942/c
LOCUS CL982942 30 bp mRNA linear GSS 21-SEP-2004
DEFINITION GC0170 TIGEM gene trap library Mus musculus cDNA clone 9125.5, mRNA sequence.
ACCESSION CL982942
VERSION CL982942.1 GI:52420370
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 30)
AUTHORS Cobellis,G., Nicolaus,G., Marra,E., Barbarisi,M., Sardiello,M., Di Giorgio,F.P., Iovino,N., Zollo,M., Ballabio,A. and Cortese,R.
TITLE Tagging genes with cassette-exchange sites
JOURNAL Unpublished (2004)
COMMENT Contact: TIGEM
107
TIGEM
Via P. Castellino, 111, 80131 NAPOLI, ITALY
Tel: +390816132205
Fax: +390815790919
Email: cobellis@tigem.it
Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from TIGEM. Annotation information available from TIGEM
Class: Gene Trap.
FEATURES Location/Qualifiers
source 1. .30
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 ola"
/db_xref="taxon:10090"
/clone="9125.5"
/sex="male"
/cell_type="Embryonic stem cell"
/cell_line="E14"
/clone_lib="TIGEM gene trap library"
/note="Vector: pFLIP1"
ORIGIN

Query Match 60.0%; Score 12.6; DB 9; Length 30;
Best Local Similarity 63.2%; Pred. No. 2.4e+05;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Qy          2 AGGACCUGCCAGUGCUCUT 20
              || |  :|||||:||:| |
Db         27 AGAATTTGCCAGTGCTCCT 9


RESULT 2
AZ821702
LOCUS       AZ821702                  28 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0094O01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0094O01 R, genomic survey sequence.
ACCESSION   AZ821702
VERSION     AZ821702.1  GI:12991610
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0094  row: O  column: 01
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 28.
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0094O01"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             58.1%;  Score 12.2;  DB 8;  Length 28;
  Best Local Similarity   58.8%;  Pred. No. 3.8e+05;
  Matches   10;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 GACCUGCCAGUGCUCUT 20
              ||||:|||| : |: :|
Db          1 GACCTGCCAATACTATT 17


RESULT 3
AG192441
LOCUS       AG192441                  28 bp    DNA     linear   GSS 06-MAR-2004
DEFINITION  Pan troglodytes DNA, clone: RP43-068P22.T7, genomic survey
            sequence.
ACCESSION   AG192441
VERSION     AG192441.1  GI:45224617
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1
  AUTHORS   Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
            Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
  TITLE     BAC end sequences of Library RP-43
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 28)
  AUTHORS   Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
            Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
            Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
            52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
            (E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
            Tel:82-42-866-7181, Fax:82-42-860-4409)
COMMENT     Clones are derived from the chimpanzee BAC library RP-43 This BAC
            end was generated during the R&D process and may have higher chance
            of clone tracking errors.
             PRIMERS
                 Sequencing: T7
             LIBRARY
                 Vector    : pBACe3.6
                 R.Site 1  : EcoRI
                 R.Site 2  : EcoRI.
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /clone="RP43-068P22.T7"
                     /sex="male"
                     /cell_type="lymphocytes"
                     /clone_lib="RP-43 Chimpanzee Male BAC Library"
ORIGIN

  Query Match             58.1%;  Score 12.2;  DB 9;  Length 28;
  Best Local Similarity   58.8%;  Pred. No. 3.8e+05;
  Matches   10;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 GGACCUGCCAGUGCUCU 19
              | || :|||| :||:|:
Db         12 GTACATGCCATTGCTCT 28


RESULT 4
AI370776/c
LOCUS       AI370776                  28 bp    mRNA    linear   EST 16-FEB-1999
DEFINITION  qz89c10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone
            IMAGE:2041746 3' similar to SW:IF4G_HUMAN Q04637 EUKARYOTIC
            TRANSLATON INITIATION FACTOR 4 GAMMA ;, mRNA sequence.
ACCESSION   AI370776
VERSION     AI370776.1  GI:4149529
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```
REFERENCE   1  (bases 1 to 28)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Insert Length: 1306   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2041746"
                     /sex="female"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="Soares_pregnant_uterus_NbHPU"
                     /note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I;
                     Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                     oligo(dT) primer [5'
                     AACTGGAAGAATTCGCGGCCGCCTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization.  Library
                     constructed by M. Fatima Bonaldo."
ORIGIN

  Query Match             55.2%;  Score 11.6;  DB 1;  Length 28;
  Best Local Similarity   61.1%;  Pred. No. 7.4e+05;
  Matches   11;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 AGGACCUGCCAGUGCUCU 19
              ||||||: |  | ||:|:
Db         20 AGGACCTACAGGCGCTCT 3


RESULT 5
AJ592231
LOCUS       AJ592231                 22 bp    DNA     linear   GSS 15-JAN-2004
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, right border, clone
            609C01, genomic survey sequence.
ACCESSION   AJ592231
VERSION     AJ592231.1  GI:37941855
KEYWORDS    GSS; right border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 22)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="609C01"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .22
                     /note="T-DNA flanking sequence
                     right border"
ORIGIN

  Query Match             52.4%;  Score 11;  DB 9;  Length 22;
  Best Local Similarity   57.9%;  Pred. No. 1.4e+06;
  Matches   11;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 GGACCUGCCAGUGCUCUTT 21
              ||  |:|||   ||:|:||
Db          3 GGGACTGCCCACGCTCTTT 21


RESULT 6
AZ847949
LOCUS       AZ847949                 29 bp    DNA     linear   GSS 21-FEB-2001
DEFINITION  2M0148B23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0148B23 R, genomic survey sequence.
ACCESSION   AZ847949
VERSION     AZ847949.1  GI:13029307
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0148  row: B  column: 23
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 29.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0148B23"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
```

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 52.4%; Score 11; DB 8; Length 29;
Best Local Similarity 57.9%; Pred. No. 1.4e+06;
Matches 11; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

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Qy          2 AGGACCUGCCAGUGCUCUT 20
              | ||||:|||  :| :| |
Db          8 ATGACCTGCCCATGATCAT 26
```

RESULT 7
AZ815857/c
LOCUS AZ815857 26 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0084A01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0084A01 F, genomic survey sequence.
ACCESSION AZ815857
VERSION AZ815857.1 GI:12985765
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 26)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0084 row: A column: 01
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 26.
FEATURES Location/Qualifiers
source 1. .26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0084A01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 51.4%; Score 10.8; DB 8; Length 26;
Best Local Similarity 64.3%; Pred. No. 1.8e+06;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Qy          8 UGCCAGUGCUCUTT 21
              :||||| | :|:||
Db         19 TGCCAGGGGTCTTT 6
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RESULT 8
AZ617463/c
LOCUS AZ617463 24 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0448F15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0448F15 R, genomic survey sequence.
ACCESSION AZ617463
VERSION AZ617463.1 GI:11739653
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0448 row: F column: 15
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
FEATURES Location/Qualifiers
source 1. .24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0448F15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 50.5%; Score 10.6; DB 8; Length 24;
Best Local Similarity 70.6%; Pred. No. 2.2e+06;
Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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Qy          2 AGGACCUGCCAGUGCUC 18
              |||| |:||||  || |
Db         18 AGGAACTGCCAACGCAC 2
```

RESULT 9
AL042578
LOCUS AL042578 28 bp mRNA linear EST 06-JUL-2004
DEFINITION DKFZp434J0821_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434J0821, mRNA sequence.
ACCESSION AL042578
VERSION AL042578.1 GI:49682446
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 28)
AUTHORS Blum,H., Bauersachs,S., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Blum, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES Location/Qualifiers
source 1. .28
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp434J0821"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN

Query Match 49.5%; Score 10.4; DB 1; Length 28;
Best Local Similarity 61.5%; Pred. No. 2.8e+06;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Qy          6 CCUGCCAGUGCUC 18
              ||:||| |: |:|
Db          3 CCTGCCNGTACTC 15
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RESULT 10
AZ642513
LOCUS AZ642513 28 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0505N01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0505N01 R, genomic survey sequence.
ACCESSION AZ642513
VERSION AZ642513.1 GI:11769194
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 28)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0505 row: N column: 01
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 28.
FEATURES Location/Qualifiers
source 1. .28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0505N01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 49.5%; Score 10.4; DB 8; Length 28;
Best Local Similarity 75.0%; Pred. No. 2.8e+06;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy          9 GCCAGUGCUCUT 20
              ||||| ||:|:|
Db          3 GCCAGAGCTCTT 14
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RESULT 11
AZ454477/c

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LOCUS       AZ454477                 29 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0256N22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0256N22 F, genomic survey sequence.
ACCESSION   AZ454477
VERSION     AZ454477.1  GI:10612602
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0256  row: N  column: 22
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 29.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0256N22"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match            49.5%;  Score 10.4;  DB 8;  Length 29;
  Best Local Similarity  75.0%;  Pred. No. 2.8e+06;
  Matches    9;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 CUGCCAGUGCUC 18
              | |||||:||:|
Db         29 CGGCCAGTGCTC 18


RESULT 12
BG424013/c
LOCUS       BG424013                 30 bp    mRNA    linear   EST 14-MAR-2001
DEFINITION  602447475F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4586106 5',
            mRNA sequence.
ACCESSION   BG424013
VERSION     BG424013.1  GI:13330519
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1314  row: e  column: 19
            High quality sequence stop: 30.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4586106"
                     /tissue_type="renal cell adenocarcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_14"
                     /note="Organ: kidney; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN

  Query Match            49.5%;  Score 10.4;  DB 4;  Length 30;
  Best Local Similarity  55.0%;  Pred. No. 2.8e+06;
  Matches   11;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 AGGACCUGCCAGUGCUCUTT 21
              || | | || | :||: :||
Db         30 AGTAACAGCAAATGCTATTT 11


RESULT 13
AZ603158/c
LOCUS       AZ603158                 22 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0422L13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0422L13 F, genomic survey sequence.
ACCESSION   AZ603158
VERSION     AZ603158.1  GI:11725348
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
```

```
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0422  row: L  column: 13
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES              Location/Qualifiers
     source           1. .22
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0422L13"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
ORIGIN

  Query Match             48.6%;  Score 10.2;  DB 8;  Length 22;
  Best Local Similarity   53.3%;  Pred. No. 3.4e+06;
  Matches    8;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          6 CCUGCCAGUGCUCUT 20
              ||: ||  :||:|:|
Db         18 CCTTCCCCTGCTCTT 4


RESULT 14
AA937308/c
LOCUS       AA937308                 28 bp    mRNA    linear   EST 10-JUN-1998
DEFINITION  om16h06.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
            IMAGE:1541243 3' similar to SW:BNC1_RAT P02683 BRAIN NEURON
            CYTOPLASMIC PROTEIN 1 ;, mRNA sequence.
ACCESSION   AA937308
VERSION     AA937308.1  GI:3095419
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Insert Length: 987   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .28
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:1541243"
                      /lab_host="DH10B"
                      /clone_lib="Soares_NFL_T_GBC_S1"
                      /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                      a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                      Equal amounts of plasmid DNA from three normalized
                      libraries (fetal lung NbHL19W, testis NHT, and B-cell
                      NCI_CGAP_GCB1) were mixed, and ss circles were made in
                      vitro. Following HAP purification, this DNA was used as
                      tracer in a subtractive hybridization reaction. The driver
                      was PCR-amplified cDNAs from pools of 5,000 clones made
                      from the same 3 libraries. The pools consisted of
                      I.M.A.G.E. clones 297480-302087, 682632-687239,
                      726408-728711, and 729096-731399. Subtraction by Bento
                      Soares and M. Fatima Bonaldo.  "
ORIGIN

  Query Match             48.6%;  Score 10.2;  DB 1;  Length 28;
  Best Local Similarity   73.3%;  Pred. No. 3.5e+06;
  Matches   11;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 AGGACCUGCCAGUGC 16
              |||| |  ||||:||
Db         28 AGGAACACCCAGTGC 14


RESULT 15
AB004341
LOCUS       AB004341                 28 bp    DNA     linear   GSS 24-JUL-1997
DEFINITION  Mouse genomic DNA, chromosome 17, clone YAC ymWIBR121D10, genomic
            survey sequence.
ACCESSION   AB004341
VERSION     AB004341.1  GI:2242909
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (sites)
  AUTHORS   Yoshino,M., Xiao,H., Jones,E., Trachtulec,Z., Vincek,V.,
            Flaherty,L. and Fischer Lindahl,K.
  TITLE     A YAC contig from the distal Mhc class I region on mouse Chr17
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 28)
  AUTHORS   Yoshino,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-MAY-1997) Masayasu Yoshino, U.T. Southwestern Medical
            Center, HHMI; 5323 Harry Hines Blvd, Dallas, TX 75235-9050, USA
            (E-mail:YOSHINO@UTSW.SWMED.EDU, Tel:214-648-5047, Fax:214-648-5453)
FEATURES              Location/Qualifiers
     source           1. .28
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /chromosome="17"
                      /clone="YAC ymWIBR121D10"
                      /haplotype="H2b"
                      /clone_lib="the MIT mouse YAC library; cat.#95021 Research
                      Genetics"
                      /note="right arm portion of the clone"
ORIGIN
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Query Match 48.6%; Score 10.2; DB 9; Length 28;
Best Local Similarity 53.3%; Pred. No. 3.5e+06;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

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Qy          5 ACCUGCCAGUGCUCU 19
              |||:|||| : |: :
Db         10 ACCTGCCACTTCTTT 24
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Search completed: September 30, 2005, 11:04:02
Job time : 2992 secs